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ART UNIT: 1652
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OM protein - protein search, using sw model

Run on: March 7, 2003, 08:41:19 ; Search time 41 Seconds

(without alignments)
2287.268 Million cell updates/sec

Title: US-09-595-526c-2

Perfect score: 11797

Sequence: 1 MACWPQLRLMKNLFFRR.....VDVAVLTSFLDEKVESYV 2261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11770	99.8	2261	1 ABC1_HUMAN	O95477 homo sapien
2	11256	95.4	2261	1 ABC1_MOUSE	P41233 mus musculu
3	5870.5	49.8	2273	1 ABCR_HUMAN	P78363 homo sapien
4	4230.5	35.9	2436	1 ABC2_HUMAN	O99207 homo sapien
5	4093.5	34.7	2434	1 ABC2_MOUSE	P41234 mus musculu
6	2642.5	22.4	1704	1 ABC3_HUMAN	O99758 homo sapien
7	1538.5	13.0	1704	1 CED7_CAEEL	P34358 caenorhabdi
8	411	3.5	330	1 DRAA_STREP	P32010 streptomyce
9	382.5	3.2	343	1 NOD1_RHISN	P55476 rhizobium s
10	366	3.1	304	1 NOD1_RHIS3	P72335 rhizobium s
11	347	2.9	308	1 YADG_ECOLI	P36879 escherichia
12	344.5	2.9	340	1 NOD1_RHIL0	P23703 rhizobium 1
13	343.5	2.9	347	1 NOD1_RHIGA	P50332 rhizobium 9
14	339.5	2.9	1280	1 MDR1_HUMAN	P08183 homo sapien
15	331.5	2.8	355	1 NOD1_RHIME	O55618 rhizobium m
16	329.5	2.8	578	1 YHHE_ECOLI	P75776 escherichia
17	327.5	2.8	1281	1 MDR3_CRIGR	P23174 cricetulus
18	327	2.8	894	1 YHHE_ECOLI	P37624 escherichia
19	326	2.8	1276	1 MDR3_MOUSE	P19844 mus musculu
20	325.5	2.8	308	1 NOSE_PSEST	P21447 mus musculu
21	324.5	2.8	1276	1 MDR2_MOUSE	P21448 mus musculu
22	322.5	2.7	306	1 NOD1_BRAJA	P26050 bradyrhizob
23	321	2.7	1276	1 MDR1_CRIGR	P21448 cricetulus
24	317	2.7	1276	1 PMD1_SCHPO	P36619 schizosacch
25	316	2.7	1276	1 MDR2_CRIGR	P21449 cricetulus
26	315.5	2.7	311	1 NOD1_RHILV	P08720 rhizobium 1
27	315	2.7	1278	1 MDR2_RAT	P43241 rattus norv
28	314.5	2.7	1278	1 MDR2_RAT	P43241 rattus norv
29	313	2.7	354	1 Y415_SYNY3	P22040 synecocyst
30	310.5	2.6	1276	1 MDR1_MOUSE	O08234 mus musculu
31	304.5	2.6	1294	1 YOH5_YEAST	O08234 saccharomyc
32	300	2.5	381	1 OPA3_BACSU	O45460 bacillus su
33	298.5	2.5	262	1 Y423_METUA	O58429 methanococc

34	297	2.5	380	1 OPCA_BACSU	O34992 bacillus su
35	296	2.5	335	1 Y719_AMASP	O05067 arabidema sp
36	293.5	2.5	1321	1 AB11_HUMAN	O95342 homo sapien
37	292.5	2.5	305	1 YHCH_BACSU	P54592 bacillus su
38	287.5	2.4	274	1 Y179_MYCPN	O50294 mycoplasma
39	286.5	2.4	274	1 Y179_MYCPE	P47425 mycoplasma
40	285.5	2.4	1279	1 MDR3_HUMAN	P21439 homo sapien
41	284	2.4	306	1 BCRA_BACLI	P42332 bacillus 11
42	284	2.4	1321	1 MDR1_CAEEL	P47112 caenorhabdi
43	284	2.4	1336	1 MAM1_SCHPO	P78966 schizosacch
44	281.5	2.4	308	1 YEHX_ECOLI	P33360 escherichia
45	281.5	2.4	343	1 ABC_ECOLI	P30750 escherichia

ALIGNMENTS

RESULT 1
ID: ABC1_HUMAN STANDARD: PRT: 2261 AA
AC: O95477; Q9UN08; Q9UN07; Q9UN06; Q9UN09; Q96T85; Q96S56;
DT: 15-OCT-2001 (Rel. 40, Created)
DT: 16-OCT-2001 (Rel. 40, Last sequence update)
DT: 15-JUN-2002 (Rel. 41, Last annotation update)
DE: ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux DE regulatory protein)
GN: ABCA1 OR ABC1 OR CERP.
OS: Homo sapiens (Human).
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX: NCBI_TaxID=9606;
RN: [1]
RP: MEDLINE=20345099; PubMed=10884428;
RA: Santamaria-Fojo S., Peterson K.M., Knapper C.L., Qiu Y., Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P., Haudenschild C.C., Prades C., Chimini G., Blackmon E.E., Francols T.L., Duverger N., Rubin E.M., Rosier M., Denelle P., Fredrickson D.S., Brewer H.B. Jr.;
RA: "Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter.";
RA: Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000). -July.
[2]
RP: TISSUE=Skin; N.A.
RA: Schwartz K., Lawn R.M., Wade D.P.;
RA: "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR.";
RA: Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP: MEDLINE=21251004; PubMed=11352567;
RA: Qiu Y., Cavelier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RA: "Human and mouse ABCA1 comparative sequencing and transgenesis studies revealing novel regulatory sequences.";
RA: Genomics 73:66-76(2001).
[4]
RP: SEQUENCE FROM N.A.
RA: Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A., Kioka N., Amachi T., Yokoyama S., Ueda K.;
RA: "A new topological model of functional human ABCA1-signal peptide cleavage and glycosylation of a large extracellular domain.";
RA: Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP: SEQUENCE OF 21-2261 FROM N.A.
RA: MEDLINE=99194349; PubMed=10092505;
RA: Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F., Chimini G., Kaminski W.E., Schmitz G.;
RA: "Molecular cloning of the human ATP-binding cassette transporter 1 (ABCA1): evidence for sterol-dependent regulation in macrophages.";
RA: Biochem. Biophys. Res. Commun. 257:29-33(1999).
[6]

- RA SEQUENCE OF 21-2261 FROM N.A.
 RX MEDLINE-99364413; PubMed-10431238;
 RA Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
 RA Delenze J.-F., Brewer H.B., Duvergier N., Deneffe P., Assmann G.;
 RT "Tangier disease is caused by mutations in the gene encoding
 RT ATP-binding cassette transporter 1.";
 RL Nat. Genet. 22:352-355(1999).
 RN [7]
 RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.
 RX MEDLINE-20001430; PubMed-10533863;
 RA Collin M., Brooks-Wilson A., Clee S.M., Rump K., Zhang L.-H., Yu L.,
 RA Collins J.A., Van Dam M., Molhuizen H.O.F., Loubser O.,
 RA Ouellette B.F.F., Sensen C.W., Fichter K., Mott S., Denis M.,
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective
 RT cholesterol efflux.";
 RL Lancet 354:1341-1346(1999).
 RN [8]
 RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.
 RX MEDLINE-99364411; PubMed-10431236;
 RA Brooks-Wilson A., Marcell M., Clee S.M., Zhang L.-H., Rump K.,
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
 RA Loubser O., Ouellette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
 RA Sensen C.W., Scherer S., Mott S., Denis M., Martindale D.,
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Mutations in ABC1 in Tangier disease and familial high-density
 RT lipoprotein deficiency.";
 RL Nat. Genet. 22:336-345(1999).
 RN [9]
 RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
 RP MET-883.
 RX MEDLINE-99364412; PubMed-10431237;
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
 RA Diederich W., Drobnik W., Barlage S., Buechler C.,
 RA Porisch-Oezcueremaz M., Kaminski W.E., Hahmann H.W., Oette K.,
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
 RT Tangier disease.";
 RL Nat. Genet. 22:347-351(1999).
 RN [10]
 RP VARIANTS TD ILE-939; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693
 RP DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
 RX MEDLINE-20540002; PubMed-11086027;
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marcell M., Rump K.,
 RA Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stult T.,
 RA Suda T., Ceeke R., Boucher B., Rondeau C., Desouch C.,
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
 RA Hayden M.R.;
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
 RT coronary artery disease in ABCA1 heterozygotes.";
 RL J. Clin. Invest. 106:1263-1270(2000).
 RN [11]
 RP VARIANTS TD ASN-1289 AND HIS-1800.
 RX MEDLINE-20171564; PubMed-10706591;
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
 RA Van Berendse P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,
 RA Vasek-Mckenna D., O'Neill G., Eberhart G.P., Weiffenbach B.,
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu Z.;
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
 RT tangier disease kindreds.";
 RL J. Lipid Res. 41:433-441(2000).
 RN [12]
 RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;
 RP ILE-825; MET-883 AND LYS-1587.
 RX MEDLINE-20396633; PubMed-10938021;
 RA Wang J., Burnett J.R., Near S., Young K., Ziman B., Hanley A.J.G.,
 RA Connelly P.W., Harris S.B., Hegde R.A.;
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
 RN [13]
 RP VARIANT TD TRP-587, AND VARIANT LEU-2168.
 RX MEDLINE-21157002; PubMed-11257260;
 RA Bertolini S., Pisciotto L., Seri M., Cusano R., Cantafora A.,
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
 RT "A point mutation in ABC1 gene in a patient with severe premature
 RT coronary heart disease and mild clinical phenotype of Tangier
 RT disease.";
 RL Atherosclerosis 154:599-605(2001).
 RN [14]
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.
 RX MEDLINE-21157003; PubMed-11257261;
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kielar D.,
 RA Pibbs S., Ordovas J.M., Aslanidis C., Lackner K.J.,
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
 RA Schmitz G.;
 RT "Common variants in the gene encoding ATP-binding cassette transporter
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.";
 RL Atherosclerosis 154:607-611(2001).
 RN [15]
 RP VARIANT TD LEU-1506.
 RX MEDLINE-21369429; PubMed-11476961;
 RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kielar D., Probst M.,
 RA Kie B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
 RA Sutrop N., Schmitz G.;
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of
 RT the ABCA1 gene and its application in genetic analysis of a new
 RT patient with familial high-density lipoprotein deficiency syndrome.";
 RL Biochim. Biophys. Acta 1537:42-48(2001).
 RN [16]
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
 RX MEDLINE-21369433; PubMed-11476965;
 RA Huang W., Moriyama K., Koga T., Hu H., Ageta M., Kawabata S.,
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;
 RT "Novel mutations in ABCA1 gene in Japanese patients with tangier
 RT disease and familial high density lipoprotein deficiency with
 RT coronary heart disease.";
 RL Biochim. Biophys. Acta 1537:71-78(2001).
 RN [17]
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.
 RX MEDLINE-21138379; PubMed-11238261;
 RA Clee S.M., Zwidderman A.H., Engert J.C., Zwarts K.Y.,
 RA Molhuizen H.O.F., Rump K., Jukema J.W., van Wiltand M., van Dam M.,
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Common genetic variation in ABCA1 is associated with altered
 RT lipoprotein levels and a modified risk for coronary artery disease.";
 RL Circulation 108:1196-1203(2001).
 RN [18]
 RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611,
 RX MEDLINE-21645894; PubMed-11785958;
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Rump K.,
 RA Ishihara M., Sakane N., Zhang Z., Tsujii K., Matsuyama A., Ohama T.,
 RA Matsuda F., Ishigami M., Sakai N., Hiraoka H., Hattori H.,
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,
 RA Yamashita S., Matsuzawa Y.;
 RT "Expression and functional analyses of novel mutations of ATP-binding
 RT cassette transporter-1 in Japanese patients with high-density
 RT lipoprotein deficiency.";
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
 CC TRANSPORT. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
 CC TRANSPORT.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN
 CC MACROPHAGES.
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
 CC ATP BINDING CASSETTE (ABC) DOMAIN.
 CC -1- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN
 CC DEFICIENCY TYPE I (HDL1), ALSO KNOWN AS TANGIER DISEASE (TD). TD
 CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY
 CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,
 CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY
 CC DISEASE (CAD).
 CC -1- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 99.8%; Score 11770; DB 1; Length 2261;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2255; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWPOLRLIMKNTLFRRRQTCQLLEVAWPLFIILIIISVLSYSPYEOHECHFPNKA 60
 DB 1 MACWPOLRLIMKNTLFRRRQTCQLLEVAWPLFIILIIISVLSYSPYEOHECHFPNKA 60
 QY 61 MPSAGTLVWVQIICNANNPCFRYPPEGAQVGVGNFNKSIYARLSARLLIYSQKDT 120
 DB 61 MPSAGTLVWVQIICNANNPCFRYPPEGAQVGVGNFNKSIYARLSARLLIYSQKDT 120
 QY 121 SMKDMKRVLTLOQIKKSSNKLQDPLVDNEFFSGFLHNLSLPKSTYDKMLRADYIIL 180
 DB 121 SMKDMKRVLTLOQIKKSSNKLQDPLVDNEFFSGFLHNLSLPKSTYDKMLRADYIIL 180
 QY 181 KYVLOGYQHLTLJLCSGSKSEEMIOLODQVSELGCPREKILAAERVLRSNMDILKPL 240
 DB 181 KYVLOGYQHLTLJLCSGSKSEEMIOLODQVSELGCPREKILAAERVLRSNMDILKPL 240
 QY 241 RLINSTSPPESKELATATKTLHSLGTLAQELFSMRSWSDMRQEVMLTNVNSSSTQI 300
 DB 241 RLINSTSPPESKELATATKTLHSLGTLAQELFSMRSWSDMRQEVMLTNVNSSSTQI 300
 QY 301 YQAVSRITVGHPRGGGLTKSLMWYEDNNYKALFPGNGTEDEAETTYDNSTFYCNDLAK 360
 DB 301 YQAVSRITVGHPRGGGLTKSLMWYEDNNYKALFPGNGTEDEAETTYDNSTFYCNDLAK 360
 QY 361 NLESSPLRIIMKALPLVGLIITPDPEATQVMAEVNKTFOELAVFDELGMEBEIS 420
 DB 361 NLESSPLRIIMKALPLVGLIITPDPEATQVMAEVNKTFOELAVFDELGMEBEIS 420
 QY 421 PKIWTWENSQENDLVRLDSDRDNHFWQQLDGLDWTADQIYAEVLAKEHEDVSSNGS 480
 DB 421 PKIWTWENSQENDLVRLDSDRDNHFWQQLDGLDWTADQIYAEVLAKEHEDVSSNGS 480
 QY 481 VYVWREAFNETNOAIRTISFMECVNLNKELEPATEVWLNKSMELDERKFNAGIYFPG 540
 DB 481 VYVWREAFNETNOAIRTISFMECVNLNKELEPATEVWLNKSMELDERKFNAGIYFPG 540
 QY 541 ITPGSIELPHHVYKIRMDIDNERTNKKIDGYWDPGPRADPFEDKRYVWGFAYLQDYY 600
 DB 541 ITPGSIELPHHVYKIRMDIDNERTNKKIDGYWDPGPRADPFEDKRYVWGFAYLQDYY 600
 QY 601 EOLIIIVLTGTEKKTGYMOQMPYPCYVDIIFLRVMSRSMPLFMTLAMIYSAVVIKGIY 660
 DB 601 EOLIIIVLTGTEKKTGYMOQMPYPCYVDIIFLRVMSRSMPLFMTLAMIYSAVVIKGIY 660
 QY 661 YEKEARLKEKRMIMGDLSILMFWSFISLIPILYSAGLLVILKIGNLLPYSDPSVPEY 720
 DB 661 YEKEARLKEKRMIMGDLSILMFWSFISLIPILYSAGLLVILKIGNLLPYSDPSVPEY 720
 QY 721 FLISVFAVNTILQCFILISTLFSRANLAAAGCIYFTLYLPYVCVAMODVGGFTLKIPAS 780
 DB 721 FLISVFAVNTILQCFILISTLFSRANLAAAGCIYFTLYLPYVCVAMODVGGFTLKIPAS 780
 QY 781 LLSPVAFGECEYFALFEEOGIGVQWNLFESEVDEDFNLJTSISMKLEDFELGYMWT 840
 DB 781 LLSPVAFGECEYFALFEEOGIGVQWNLFESEVDEDFNLJTSISMKLEDFELGYMWT 840
 QY 841 YIEAVPFGOGYIPRPWFPCYKSYWFGESDEKSHPSQNKRSSEICMEEPHKLIGVS 900
 DB 841 YIEAVPFGOGYIPRPWFPCYKSYWFGESDEKSHPSQNKRSSEICMEEPHKLIGVS 900
 QY 901 IONLVKVRDGMVAVDGLANLFEYQITSLFNGHNGAGKTTMSILTLGPPPTSGATYIL 960
 DB 901 IONLVKVRDGMVAVDGLANLFEYQITSLFNGHNGAGKTTMSILTLGPPPTSGATYIL 960
 QY 961 GKIRISEMSTIRONLGYCPOHNVLFDMILVEEHIWFAYLKGLSEKHVKAEMQMLDVG 1020
 DB 961 GKIRISEMSTIRONLGYCPOHNVLFDMILVEEHIWFAYLKGLSEKHVKAEMQMLDVG 1020

QY 1021 LPSSKLKSTQSLSGGMKRLSVLALFVGSKVYILDEPAGADVPYRRGIWELLKYRQ 1080
 DB 1021 LPSSKLKSTQSLSGGMKRLSVLALFVGSKVYILDEPAGADVPYRRGIWELLKYRQ 1080
 QY 1081 GRTIILSTHMEDEADVLDGRIIAIISHGKLCVGSSEFLKNOLOGTYLTLVKKVBESSLS 1140
 DB 1081 GRTIILSTHMEDEADVLDGRIIAIISHGKLCVGSSEFLKNOLOGTYLTLVKKVBESSLS 1140
 QY 1141 SCRNSSSTVSYLKKEDSVSSSDAGLGSDESOTLTIDVSAISNLRKHVSEARLVEDI 1200
 DB 1141 SCRNSSSTVSYLKKEDSVSSSDAGLGSDESOTLTIDVSAISNLRKHVSEARLVEDI 1200
 QY 1201 GHELTYYVLYPEAKEGAEVLEFHEIDRLSDLGISSYGISSETTLEBIFLKYAESGVDAE 1260
 DB 1201 GHELTYYVLYPEAKEGAEVLEFHEIDRLSDLGISSYGISSETTLEBIFLKYAESGVDAE 1260
 QY 1261 TSDGTLPARRRRRRAFGKQOSOLREFTEDDAADPNDSDIDPESRETDLSGMDGKSYQVK 1320
 DB 1261 TSDGTLPARRRRRRAFGKQOSOLREFTEDDAADPNDSDIDPESRETDLSGMDGKSYQVK 1320
 QY 1321 GMLTQOQFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVSLIYPPGKYPSLELO 1380
 DB 1321 GMLTQOQFVALLMKRLIARRSRKGFPAQIVLPAVFCIALVSLIYPPGKYPSLELO 1380
 QY 1381 PMWNEQYTFVSNDAPEBDTGLELLNALTKDPGEGTRCMENP1PDTPCQAGEBEMTAP 1440
 DB 1381 PMWNEQYTFVSNDAPEBDTGLELLNALTKDPGEGTRCMENP1PDTPCQAGEBEMTAP 1440
 QY 1441 VPOTIMDLFONGNMTMOPSPACOSSDKIKKMLPVCPCPGGGLPPOROKONTADIIQDL 1500
 DB 1441 VPOTIMDLFONGNMTMOPSPACOSSDKIKKMLPVCPCPGGGLPPOROKONTADIIQDL 1500
 QY 1501 TGRNISDYLVNTYQYIINKSLKNKIWNEFFRYGGSLSVSTQALPQOEVDNDAIKOMK 1560
 DB 1501 TGRNISDYLVNTYQYIINKSLKNKIWNEFFRYGGSLSVSTQALPQOEVDNDAIKOMK 1560
 QY 1561 HIKLAKDSSADRFNLNSLGRFMTGDTBRNNVKEFNKMKWHAISSFLVANNAILIRANLOK 1620
 DB 1561 HIKLAKDSSADRFNLNSLGRFMTGDTBRNNVKEFNKMKWHAISSFLVANNAILIRANLOK 1620
 QY 1621 GENPSHYGITAFAFNHPLNLTQOOLSEVALMTTSVYLVASICYIFMSPFPAFVFFLQER 1680
 DB 1621 GENPSHYGITAFAFNHPLNLTQOOLSEVALMTTSVYLVASICYIFMSPFPAFVFFLQER 1680
 QY 1681 VSKAKHLOFISGVKPIVIMLSNFWDMKCNVYVPAVLIIIFICRQOKSVYSTNLPYAL 1740
 DB 1681 VSKAKHLOFISGVKPIVIMLSNFWDMKCNVYVPAVLIIIFICRQOKSVYSTNLPYAL 1740
 QY 1741 LLLYGSITPLMPASVEFKIPSTAYVVLVSVNLFGINGSVATFVLEFTDKLNNIN 1800
 DB 1741 LLLYGSITPLMPASVEFKIPSTAYVVLVSVNLFGINGSVATFVLEFTDKLNNIN 1800
 QY 1801 DILKSVFLIFPFCIGRLIDMVKNQAMADALEPGENRFPSPISMDLYGNLIRAMAVEG 1860
 DB 1801 DILKSVFLIFPFCIGRLIDMVKNQAMADALEPGENRFPSPISMDLYGNLIRAMAVEG 1860
 QY 1861 VVEFLITVLIQYREFIRRPYNAKLSPLUNDEDEYRREORQILIDGGGONDLIEIKELTKI 1920
 DB 1861 VVEFLITVLIQYREFIRRPYNAKLSPLUNDEDEYRREORQILIDGGGONDLIEIKELTKI 1920
 QY 1921 YRRKRPAYVDRICVQIPGECFGLGVNAGAKSSSTFKMLTGTDTVTRGDAFLNKNISLSN 1980
 DB 1921 YRRKRPAYVDRICVQIPGECFGLGVNAGAKSSSTFKMLTGTDTVTRGDAFLNKNISLSN 1980
 QY 1981 IHEVQNNNGYCPOPATIELLIGREHVEFFALLGVPEKEKGKGEVNAIRKLGIVYKGEK 2040
 DB 1981 IHEVQNNNGYCPOPATIELLIGREHVEFFALLGVPEKEKGKGEVNAIRKLGIVYKGEK 2040
 QY 2041 YAGNTSGNKRRLSTAMALIGPPVYFLEDEPTTGMDEKARFLLNICALSVYKEGRSVLT 2100
 DB 2041 YAGNTSGNKRRLSTAMALIGPPVYFLEDEPTTGMDEKARFLLNICALSVYKEGRSVLT 2100
 QY 2101 SHSMECEALCTRMAIMVNGRFRCLGYSVQHLKNRRFGDGYITVIRIAGSNPDLKPVODFFG 2160

QY 241 RTLNSTSPSPSKELAEATKTLHSLGTLAQELFSMRSMKROEVMPLTNVSSSSSTOI 300
 Db 241 RLNSTSPSPSKELAEATKTLHSLGTLAQELFSMRSMKROEVMPLTNVSSSSSTOI 300
 QY 301 YQAVRIVYCGHPEGGLKIKSLNMYEDNNYKALFGNGCTEEDAEFTYDNSTPYCNDLMM 360
 Db 301 YQAVRIVYCGHPEGGLKIKSLNMYEDNNYKALFGNGCTEEDAEFTYDNSTPYCNDLMM 360
 QY 361 NLESPSLRILMKALPKLLVKKIITPTPATROYMAEVNKTFOELAVFHDLESMWELS 420
 Db 361 NLESPSLRILMKALPKLLVKKIITPTPATROYMAEVNKTFOELAVFHDLESMWELS 420
 QY 421 PKWTFMENSOEMDLVRLDSDRNDHFWEQDLGDMTADIDYAFIAKHEDEVOSNGS 480
 Db 421 PKWTFMENSOEMDLVRLDSDRNDHFWEQDLGDMTADIDYAFIAKHEDEVOSNGS 480
 QY 481 VYTRREAFENETNOAIRISRENECVNLKLEPIATEVWLINRSMELLDERKFMAGIVFTG 540
 Db 481 VYTRREAFENETNOAIRISRENECVNLKLEPIATEVWLINRSMELLDERKFMAGIVFTG 540
 QY 541 ITPGSEILPHVKKIKRMDIDNVEETNKIKDGYWDPGRADPFEDMRYWVGCFAYLODVY 600
 Db 541 ITPGSEILPHVKKIKRMDIDNVEETNKIKDGYWDPGRADPFEDMRYWVGCFAYLODVY 600
 QY 601 EOAIIIRVLGTEKKTGYVMOOMPYPYVDIIFLRVMSRSMPLFMTLAMIYSVAIIKGIY 660
 Db 601 EOAIIIRVLGTEKKTGYVMOOMPYPYVDIIFLRVMSRSMPLFMTLAMIYSVAIIKGIY 660
 QY 661 YEKARLKEPMIRINGLDNLSIMFSWISLIPDLVSAGLLVILIKGNLLPYSDPSVVEY~720
 Db 661 YEKARLKEPMIRINGLDNLSIMFSWISLIPDLVSAGLLVILIKGNLLPYSDPSVVEY~720
 QY 721 FLVSFAVVTLLQCLISTLFSRANLAAAGGIIYFTLLVYLCVAMODVVGFTLKIFAS 780
 Db 721 FLVSFAVVTLLQCLISTLFSRANLAAAGGIIYFTLLVYLCVAMODVVGFTLKIFAS 780
 QY 781 LLSVAFGFCETPALFEEOGIGVOMDNLESPVEEDGFNLMTSISAMLEDFLYGMVW 840
 Db 781 LLSVAFGFCETPALFEEOGIGVOMDNLESPVEEDGFNLMTSISAMLEDFLYGMVW 840
 QY 841 YIEAVPFGOGIPRPWFYFCTKSWRGESEDEKSHPSNOKRMSLCEMEEPHILKIGVS 900
 Db 841 YIEAVPFGOGIPRPWFYFCTKSWRGESEDEKSHPSNOKRMSLCEMEEPHILKIGVS 900
 QY 901 IONLVKYYRDMKVAVDGLALNFYEQITSLFHNAGKTTMSILTGLPPTSGRAYTL 960
 Db 901 IONLVKYYRDMKVAVDGLALNFYEQITSLFHNAGKTTMSILTGLPPTSGRAYTL 960
 QY 961 GKDIRSMSTIRONLGVCPQHNVLFDMLVIEEHIWYARLKGISEKHVAKEMQMLDVG 1020
 Db 961 GKDIRSMSTIRONLGVCPQHNVLFDMLVIEEHIWYARLKGISEKHVAKEMQMLDVG 1020
 QY 1021 LPSKLSKSKTSQSGGOKRLSYALAFVGGSKYVILDEPTAGDPYSRGIMWELLYKQ 1080
 Db 1021 LPSKLSKSKTSQSGGOKRLSYALAFVGGSKYVILDEPTAGDPYSRGIMWELLYKQ 1080
 QY 1081 GRTIILSTHMEADYVLDGRIALISHGKLCVGSFLKNQLOTOGYTLVYKEDVSSLS 1140
 Db 1081 GRTIILSTHMEADYVLDGRIALISHGKLCVGSFLKNQLOTOGYTLVYKEDVSSLS 1140
 QY 1141 SCNNSSSTVYLLKEDSVOSSSDAGLGSDESSTLTIVSAISNLRKHVSEARLVEDI 1200
 Db 1141 SCNNSSSTVYLLKEDSVOSSSDAGLGSDESSTLTIVSAISNLRKHVSEARLVEDI 1200
 QY 1201 GHELTAVLYEAKEGAFELFEIDRLSDGISSYSETTLEIFLKVAEESVDAE 1260
 Db 1201 GHELTAVLYEAKEGAFELFEIDRLSDGISSYSETTLEIFLKVAEESVDAE 1260
 QY 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSIDIPESRETDLLSGMGKGSYQVK 1320
 Db 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSIDIPESRETDLLSGMGKGSYQVK 1320
 1321 GMLTQOQGVALLMKRLILARRSKGFFAQIYLPVAFVCIALVFSIYPPFGKYSLEIQ 1380

Db 1321 GMLTQOQGVALLMKRLILARRSKGFFAQIYLPVAFVCIALVFSIYPPFGKYSLEIQ 1380
 QY 1381 PMYNQOYTFVSNDADEDTGTELLNALTKDGFGRGCRMEGNIPTPCQAGEEEMTAP 1440
 Db 1381 PMYNQOYTFVSNDADEDTGTELLNALTKDGFGRGCRMEGNIPTPCQAGEEEMTAP 1440
 QY 1441 VPOTIMDLFONGMWTQONSPACOSSDKIKKMLPCPAGAGLPPQOKONTAIIODL 1500
 Db 1441 VPOTIMDLFONGMWTQONSPACOSSDKIKKMLPCPAGAGLPPQOKONTAIIODL 1500
 QY 1501 TGRNIDSLVKTYYVOIIANSKKNKWNEFRYGEFSLGVSNTQALPPSEVDAIKOMK 1560
 Db 1501 TGRNIDSLVKTYYVOIIANSKKNKWNEFRYGEFSLGVSNTQALPPSEVDAIKOMK 1560
 QY 1561 HILKADSSADREFLNSLGFPMGTIDTRNNVAKWFPNNKGHAISSELYNINNALIRANLOK 1620
 Db 1561 HILKADSSADREFLNSLGFPMGTIDTRNNVAKWFPNNKGHAISSELYNINNALIRANLOK 1620
 QY 1621 GENPSHYGITAFNRHRLNLTQOOLSEVALMTTSVDVLSICVIFAMSPYBASVVFLOER 1680
 Db 1621 GENPSHYGITAFNRHRLNLTQOOLSEVALMTTSVDVLSICVIFAMSPYBASVVFLOER 1680
 QY 1681 VSKAKHLOFISGVKPYIYVLSNFWDMCNVVPATLVIIIFCFOOKSVSSTNLPLVAL 1740
 Db 1681 VSKAKHLOFISGVKPYIYVLSNFWDMCNVVPATLVIIIFCFOOKSVSSTNLPLVAL 1740
 QY 1741 LLLLYGMSITPLMYPASPEFKJESTAYVVLVSYNLFICINGSVAFFVLELFTDKNLININ 1800
 Db 1741 LLLLYGMSITPLMYPASPEFKJESTAYVVLVSYNLFICINGSVAFFVLELFTDKNLININ 1800
 QY 1801 DILKSVELIIPHFCLGRGLIDMKVKNQAMADALERGENREVSPLSMDLVGRNLFMAVEG 1860
 Db 1801 DILKSVELIIPHFCLGRGLIDMKVKNQAMADALERGENREVSPLSMDLVGRNLFMAVEG 1860
 QY 1861 VVEFLITVLIQYREFIRRPVNAKLSPLNDEDEYRERORILIDGGONDILEIKELTKI 1920
 Db 1861 VVEFLITVLIQYREFIRRPVNAKLSPLNDEDEYRERORILIDGGONDILEIKELTKI 1920
 QY 1921 YRRKRPAYDRICVGIIPGEGCGLLGVNAGAKSSTFKMLTDDTTRDADALNNKSTLSN 1980
 Db 1921 YRRKRPAYDRICVGIIPGEGCGLLGVNAGAKSSTFKMLTDDTTRDADALNNKSTLSN 1980
 QY 1981 IHEVQNNKGYCOPDPAITELLTGREHVEFFALLRGVPERKEVKGEMAIRKLGIVKGEK 2040
 Db 1981 IHEVQNNKGYCOPDPAITELLTGREHVEFFALLRGVPERKEVKGEMAIRKLGIVKGEK 2040
 QY 2041 YAGNYSGGNKRRLSTAMLLIGGPPVFIIDEPYTGMDPRARFLNICALSVYKEGRSVLT 2100
 Db 2041 YAGNYSGGNKRRLSTAMLLIGGPPVFIIDEPYTGMDPRARFLNICALSVYKEGRSVLT 2100
 QY 2101 SHSMECEALCTRMAIMVNGFRCLGSVOHLKNRFGDDYITVIRIASSNPDLKRVODPFG 2160
 Db 2101 SHSMECEALCTRMAIMVNGFRCLGSVOHLKNRFGDDYITVIRIASSNPDLKRVODPFG 2160
 QY 2161 LAFPSVYLKEXHRNMLQYOLPSSLSLARIFSILSOSKKRLIHEDYSVQTTIDOVFNF 2220
 Db 2161 LAFPSVYLKEXHRNMLQYOLPSSLSLSLARIFSILSOSKKRLIHEDYSVQTTIDOVFNF 2220
 QY 2221 AKDQSDDDLKDLSLHKNQYVDAVAVLTSFLQDEKVESYV 2261
 Db 2221 AKDQSDDDLKDLSLHKNQYVDAVAVLTSFLQDEKVESYV 2261

RESULT 2

US-09-846-456-11

Sequence 11, Application us/09846456

Patent No. US20020146792A1

GENERAL INFORMATION:

APPLICANT: Koster, Marie

APPLICANT: Prades, Catherine

APPLICANT: Lemoine, Cendrine

APPLICANT: Naudin, Laurent

APPLICANT: Deneffe, Patrice
 APPLICANT: Duveger, Nicolas
 APPLICANT: Brewer, Bryan
 APPLICANT: Remaley, Alan
 APPLICANT: Fojo, Silvia
 TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
 TITLE OF INVENTION: Activity and Therapeutic Uses
 FILE REFERENCE: 3806.0505
 CURRENT APPLICATION NUMBER: US/09/846,456
 CURRENT FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: US 60/201,280
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patent version 3.0
 SEQ ID NO 11
 LENGTH: 2261
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-846-456-11

Query Match 99.7%; Score 11767; DB 10; Length 2261;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2254; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACWPOLRLILMKNLFRFRROTQQLLEVAWPLFLLILSVRLSTPYEQHECHFPNKA 60
 DB 1 MACWPOLRLILMKNLFRFRROTQQLLEVAWPLFLLILSVRLSTPYEQHECHFPNKA 60
 QY 61 MPAGLPLWVQGITCANNPCFRPTPGGAPGVGNPNSTVARLPSDARLLLYSOKRT 120
 DB 61 MPAGLPLWVQGITCANNPCFRPTPGGAPGVGNPNSTVARLPSDARLLLYSOKRT 120
 QY 121 SMKDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 DB 121 SMKDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 QY 121 SMKDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 DB 121 SMKDMKRVLTLOQIKKSSNLKLOELVDNENFSGFLYHNLSPKSTYDKMLRADVILH 180
 QY 181 KYVLOGYQHLTSLCNGSSEEMIOUGDOEVSFLCGLPEKLAARVLRSMNDILKPTL 240
 DB 181 KYVLOGYQHLTSLCNGSSEEMIOUGDOEVSFLCGLPEKLAARVLRSMNDILKPTL 240
 QY 241 RTLNSTSPPSKELATATTLTSLGTLAOLFSMRSWSDMROEVMFLNNVSSSSSTOI 300
 DB 241 RTLNSTSPPSKELATATTLTSLGTLAOLFSMRSWSDMROEVMFLNNVSSSSSTOI 300
 QY 301 YOAVSRIVCGHPEGGGLIKSLNMYEDNNYKALFGNGTEDEATFTYDSTTPYCNDLAK 360
 DB 301 YOAVSRIVCGHPEGGGLIKSLNMYEDNNYKALFGNGTEDEATFTYDSTTPYCNDLAK 360
 QY 361 NLESPLSLRIYKALKPLVGLKLLYPTDPATROVNAEVNKTFOELAVFHDLGMEWELS 420
 DB 361 NLESPLSLRIYKALKPLVGLKLLYPTDPATROVNAEVNKTFOELAVFHDLGMEWELS 420
 QY 421 PKIWTENSOEEDLVRLMLDSRDNDHFEQOGLDMTAAODIVARLAHHPEDVOSSNS 480
 DB 421 PKIWTENSOEEDLVRLMLDSRDNDHFEQOGLDMTAAODIVARLAHHPEDVOSSNS 480
 QY 481 VYTWRAFAFNETNOAIFRTISFMECVNLKLEPATEVWLINKSMELDERKKEWAGIVFTG 540
 DB 481 VYTWRAFAFNETNOAIFRTISFMECVNLKLEPATEVWLINKSMELDERKKEWAGIVFTG 540
 QY 541 ITPGSELPHHYKYKTRMDIDNERENKTKDGYWDPGRADPEDRMRYWGGGAYLQDYY 600
 DB 541 ITPGSELPHHYKYKTRMDIDNERENKTKDGYWDPGRADPEDRMRYWGGGAYLQDYY 600
 QY 601 EOAIIIVLTGTEKKTGVYMOQMPYCYVDIDFLRVSRSMLPMTLAWIYSAVIAIKGIV 660
 DB 601 EOAIIIVLTGTEKKTGVYMOQMPYCYVDIDFLRVSRSMLPMTLAWIYSAVIAIKGIV 660
 QY 661 YEAEALKEFMRLMGDNLSTLWFSWISSILPLVLSAGLLVILKGNLLPYSDPSVFEV 720
 DB 661 YEAEALKEFMRLMGDNLSTLWFSWISSILPLVLSAGLLVILKGNLLPYSDPSVFEV 720
 QY 721 FLVSFAVVTILQCFILSTLFSRANLAACGGIITFTLYLTPYVLCVAMODYVGGFTLKIFAS 780

DB 721 FLVSFAVVTILQCFILSTLFSRANLAACGGIITFTLYLTPYVLCVAMODYVGGFTLKIFAS 780
 QY 781 LLSPAFGGCEYFALFEEOGIGVOMDNLFPVEBDCFNLTISMLPDTLYGWTW 840
 DB 781 LLSPAFGGCEYFALFEEOGIGVOMDNLFPVEBDCFNLTISMLPDTLYGWTW 840
 QY 841 YIEAFPCQYIGIPRWYPCCKSWFGESEDEKSHPGSNOKRMEICMEEPPTLKIGVS 900
 DB 841 YIEAFPCQYIGIPRWYPCCKSWFGESEDEKSHPGSNOKRMEICMEEPPTLKIGVS 900
 QY 901 IONLVKVRDGMKVAVDGLALNFYEGQITTSFLGHNGAGKTTMSILTGPPPTSGTAYIL 960
 DB 901 IONLVKVRDGMKVAVDGLALNFYEGQITTSFLGHNGAGKTTMSILTGPPPTSGTAYIL 960
 QY 961 GKDIKSEMTIRONLGVCPORHNVLFDMLTVEHEHIFARLKLSEKHVKAEMEQMALDVG 1020
 DB 961 GKDIKSEMTIRONLGVCPORHNVLFDMLTVEHEHIFARLKLSEKHVKAEMEQMALDVG 1020
 QY 1021 LPSSKLKSKTSOLSGMOKRLSVLAFVGSKVYILDEPTAGVDPYRRGIMELLKYRQ 1080
 DB 1021 LPSSKLKSKTSOLSGMOKRLSVLAFVGSKVYILDEPTAGVDPYRRGIMELLKYRQ 1080
 QY 1081 GRTIILSTHMDADVLGDRIAIISHGKLCVGSFLKNOLGTYVLTLYKKDVESLS 1140
 DB 1081 GRTIILSTHMDADVLGDRIAIISHGKLCVGSFLKNOLGTYVLTLYKKDVESLS 1140
 QY 1141 SCRNSSSTVSLKKEDESVSSSDAGLSGDSHESDTLTIDVSAISNLRKHVSEARLYEDI 1200
 DB 1141 SCRNSSSTVSLKKEDESVSSSDAGLSGDSHESDTLTIDVSAISNLRKHVSEARLYEDI 1200
 QY 1201 GHELTYYVPEAAKEGAVELFHEIDRLSDLGISVIGSTTLEETFLKAAEESGDVE 1260
 DB 1201 GHELTYYVPEAAKEGAVELFHEIDRLSDLGISVIGSTTLEETFLKAAEESGDVE 1260
 QY 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSDIPESRETDLSCMDGSGSYOVK 1320
 DB 1261 TSDGTLPARRRNRAFGDKOSCLRPFTEDDAADPNDSDIPESRETDLSCMDGSGSYOVK 1320
 QY 1321 GSKLTQOQFVALMKRLLIARRSRKGFPAQIVLPAVFCIALVPSLIVPPGKYPSELO 1380
 DB 1321 GSKLTQOQFVALMKRLLIARRSRKGFPAQIVLPAVFCIALVPSLIVPPGKYPSELO 1380
 QY 1381 PMYNEQYTFVSNDAPEDTGTLELNLTKDPGFTQCMESNPIDPDPQAGEEWTTAP 1440
 DB 1381 PMYNEQYTFVSNDAPEDTGTLELNLTKDPGFTQCMESNPIDPDPQAGEEWTTAP 1440
 QY 1441 VPOTIMDLFONGNMTMNPSPACOCSSDKIKMLPVCPPAGGLPPOQRKONTADILQDL 1500
 DB 1441 VPOTIMDLFONGNMTMNPSPACOCSSDKIKMLPVCPPAGGLPPOQRKONTADILQDL 1500
 QY 1501 TGRNLSDLVTKTYQIILAKSLKNKIWNEFRYGGFSLGVSNTQALPPSOEYNDAIKQMK 1560
 DB 1501 TGRNLSDLVTKTYQIILAKSLKNKIWNEFRYGGFSLGVSNTQALPPSOEYNDAIKQMK 1560
 QY 1561 HLKLAQDSADRFNLNLSLGRFMTGLDTRNNVYKVPNNKGWHAISFFLVNINAILRANLQK 1620
 DB 1561 HLKLAQDSADRFNLNLSLGRFMTGLDTRNNVYKVPNNKGWHAISFFLVNINAILRANLQK 1620
 QY 1621 GENPSHYGITAFNHPNLNLTQOOLSEVALMTTSDVLYSICVIFAMSFVPASVFLIOER 1680
 DB 1621 GENPSHYGITAFNHPNLNLTQOOLSEVALMTTSDVLYSICVIFAMSFVPASVFLIOER 1680
 QY 1681 VSKAKHLOFISGVAPVYIWLNSFWMDKCNVVPATLYIIIFICQOQSYSTSTLPLVAL 1740
 DB 1681 VSKAKHLOFISGVAPVYIWLNSFWMDKCNVVPATLYIIIFICQOQSYSTSTLPLVAL 1740
 QY 1741 LLLYGSWITPLMYPASEVFKIPSTAVVLTAVNLFGINGSVATFVLELFTDKNLNIN 1800
 DB 1741 LLLYGSWITPLMYPASEVFKIPSTAVVLTAVNLFGINGSVATFVLELFTDKNLNIN 1800
 QY 1801 DILKSVLIFPHFCLGRLLIMYKNAQAAALBEPGENREYSPSLMDLVGRNLPAMAPEG 1860

Db 1801 DLKSVFLIPHPHCLGSLDMKKNAMADALEFGENREVSPLSWDLVGRNLPMAAVEG 1860
Qy 1861 VVFLITLVLIQYREFIRPRVNAKLSPLENDEDEDVRRERORILLDGGONDILEIKELTKI 1920
Db 1861 VVFLITLVLIQYREFIRPRVNAKLSPLENDEDEDVRRERORILLDGGONDILEIKELTKI 1920
Qy 1921 YRRKRKAVDRICVIGTIPGECFGLSYNGAGKSTFEMLTGDTTTRGDAFLKNSTLSN 1980
Db 1921 YRRKRKAVDRICVIGTIPGECFGLSYNGAGKSTFEMLTGDTTTRGDAFLKNSTLSN 1980
Qy 1981 IHEHONMGCPQPDATITELTGREHEFPALLRGVPERKVGKVGEMATIKLILVYGEK 2040
Db 1981 IHEHONMGCPQPDATITELTGREHEFPALLRGVPERKVGKVGEMATIKLILVYGEK 2040
Qy 2041 YAGNYSGNKRLSTAMALIGPPVFLDEPTTGMDPKARFLMNCALSVYKGRSVLT 2100
Db 2041 YAGNYSGNKRLSTAMALIGPPVFLDEPTTGMDPKARFLMNCALSVYKGRSVLT 2100
Qy 2101 SHSMECEALCTRAIMVNRFRCLSGVQHLKRRGDTTIVRIAGSNPDLKPVODFG 2160
Db 2101 SHSMECEALCTRAIMVNRFRCLSGVQHLKRRGDTTIVRIAGSNPDLKPVODFG 2160
Qy 2161 LAEPGSLKRRHMLQYOLPSSLSLARIESTLSOSKRLHEDYSVQTLIDVYVNF 2220
Db 2161 LAEPGSLKRRHMLQYOLPSSLSLARIESTLSOSKRLHEDYSVQTLIDVYVNF 2220
Qy 2221 AKDOSDDHLKDLSLKRNQTVVAVVLTSPLODEKYESY 2261
Db 2221 AKDOSDDHLKDLSLKRNQTVVAVVLTSPLODEKYESY 2261

RESULT 3

US-09-595-542-9
Sequence 9, Application US/0995542
Patent No. US20020127647A1
GENERAL INFORMATION:
APPLICANT: Shutter, John
TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
FILE REFERENCE: 00-658-A
CURRENT APPLICATION NUMBER: US/09/995,542
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/253,520
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2201
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: UNSURE
LOCATION: (115)
OTHER INFORMATION: amino acid at this position is unknown
US-09-995-542-9

Query Match 92.6%; Score 10922; DB 10; Length 2201;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 2089; Conservative 55; Mismatches 57; Indels 0; Gaps 0;

Qy 61 MSAGLTPVVGIGICNANPCFRYPTEGAPGVGNFNKSIYARLESARLLILYSQKDT 120
Db 1 MSAGLTPVVGIGICNANPCFRYPTEGAPGVGNFNKSIYARLESARLLILYSQKDT 60
Qy 121 SKMDKRVLTQOQIKSSSNKLDDELVDNTEFSGFLYHNLSLKRSYDQKLADVILH 180
Db 121 SKMDKRVLTQOQIKSSSNKLDDELVDNTEFSGFLYHNLSLKRSYDQKLADVILH 120
Qy 61 STKDHAKVLRMLQIKHPSNKLQDFLDVNDTEFSGFLQHNLSLPRSTYDLSQXNVG 120
Db 61 STKDHAKVLRMLQIKHPSNKLQDFLDVNDTEFSGFLQHNLSLPRSTYDLSQXNVG 120
Qy 181 KYFLOGYOLHLTSLGSKSEEMIOGLDOVESELGLPEKRIAAERVLRSMNLTLP 240
Db 121 KYFLOGYOLHLTSLGSKSEEMIOGLDOVESELGLPEKRIAAERVLRSMNLTLP 180

Qy 241 PTLNSTPPSPKELAEATKTLTSLGTLAOLFLFSRMSNDKROEMFLTNVSSSSSTOI 300
Db 181 TKLNTSHLPQHLAEATKTLTSLGTLAOLFLFSRMSNDKROEMFLTNVSSSSSTOI 240
Qy 301 YQAVSRVCGHEGGGLIKSLMWYEDNNYKALFEGNGTEDEATFYDNSTPYCNDLMK 360
Db 241 YQAVSRVCGHEGGGLIKSLMWYEDNNYKALFEGNGTEDEATFYDNSTPYCNDLMK 300
Qy 361 NLESSPLSLIKALKPLVGLKILTPPTPATROYMAEVNKTPOBLAVHDLJEGMBELS 420
Db 301 NLESSPLSLIKALKPLVGLKILTPPTPATROYMAEVNKTPOBLAVHDLJEGMBELS 360
Qy 421 PKITWEMENSOEMDLYRMLDSRODNHFWEOOLGDMTADIDYAFIAKHEDEVOSSNGS 480
Db 361 PKITWEMENSOEMDLYRMLDSRODNHFWEOOLGDMTADIDYAFIAKHEDEVOSSNGS 420
Qy 481 VYTWREAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIYFTG 540
Db 421 VYTWREAFNETNOAIRTISREMECVNLKLEPIATEVWLINKSMELDERKFMAGIYFTG 480
Qy 541 ITPGSELPHHYKTKRNDIDNERTNKIKDGYWDPGRADPFEDMRVWGFAYLQDV 600
Db 481 ITPGSELPHHYKTKRNDIDNERTNKIKDGYWDPGRADPFEDMRVWGFAYLQDV 540
Qy 601 EOAIRVLTGTEKKTGYVMQMPYPCYVDLFLVMSKSMPLFMTLAMIYSVANIITGIV 660
Db 541 EOAIRVLTGTEKKTGYVMQMPYPCYVDLFLVMSKSMPLFMTLAMIYSVANIITGIV 600
Qy 661 YEKARLKETMRIMGLDINSILFESNLSLPLVSAGLVILKGLNLPLSPSPVAVF 720
Db 601 YEKARLKETMRIMGLDINSILFESNLSLPLVSAGLVILKGLNLPLSPSPVAVF 660
Qy 721 FLVSAAVVTIIQCFILSTLFSRANLAAAGGIIFTYLPVLCVAMQDYVGTFLKIFAS 780
Db 661 FLVSAAVVTIIQCFILSTLFSRANLAAAGGIIFTYLPVLCVAMQDYVGTFLKIFAS 720
Qy 781 LLSPPAFGCEYFALPFGOGIGVOMDNLFPSPYEEOGNLTITSIMMLDTPLYGWTW 840
Db 721 LLSPPAFGCEYFALPFGOGIGVOMDNLFPSPYEEOGNLTITSIMMLDTPLYGWTW 780
Qy 841 YIEAVFQOYGIIPRWYFPCTKSYWFEESDEKSHPSNOKRMEISEMEDEPTLKGVS 900
Db 781 YIEAVFQOYGIIPRWYFPCTKSYWFEESDEKSHPSNOKRMEISEMEDEPTLKGVS 840
Qy 901 IONLVKVRDGMKVAVDGLALNFEGOTTSLGHNGAKTTTSLTGLPPTSGATYL 960
Db 841 IONLVKVRDGMKVAVDGLALNFEGOTTSLGHNGAKTTTSLTGLPPTSGATYL 900
Qy 961 GKDIRSEKSTIRONLGYCPOHNVLFDMLTVEHIMFYARLKSEKRVKAEQOMALDVG 1020
Db 901 GKDIRSEKSTIRONLGYCPOHNVLFDMLTVEHIMFYARLKSEKRVKAEQOMALDVG 960
Qy 1021 LPSSKLKSKTSQLSGGMQRLSVLALFVGSKVYIIDEPTAGVDPYRRRIWELLKRYQ 1080
Db 961 LPSSKLKSKTSQLSGGMQRLSVLALFVGSKVYIIDEPTAGVDPYRRRIWELLKRYQ 1020
Qy 1081 GRTIILSTHHNDEADVIGDRALISHRKLCVSSSFLKMQDGTGYLLLVKKDVESSLS 1140
Db 1021 GRTIILSTHHNDEADVIGDRALISHRKLCVSSSFLKMQDGTGYLLLVKKDVESSLS 1080
Qy 1141 SCRNSSTVSTLKKEDESVSSSDAGSGSHESPTLIDVSAISNLIRKVSARLVED 1200
Db 1081 SCRNSSTVSTLKKEDESVSSSDAGSGSHESPTLIDVSAISNLIRKVSARLVED 1140
Qy 1201 GHELTLYVLYEAKAGAFVELFHEIDRLSDLGSSYGISSETTLEETFLKVAEESGDAE 1260
Db 1141 GHELTLYVLYEAKAGAFVELFHEIDRLSDLGSSYGISSETTLEETFLKVAEESGDAE 1200
Qy 1261 TSDGTLPARNRRAFGKQSCLPFTEDADAPNDSDIDPESRETDLLSGMDGKSGSYQK 1320
Db 1201 TSDGTLPARNRRAFGKQSCLPFTEDADAPNDSDIDPESRETDLLSGMDGKSGSYQK 1260
Qy 1321 GMLTQOQFVALLMKRLLIARSRKGFQIVLPAVFCIALVFSLIVPPFGKRYPSLEIQ 1380